Serial Number: _10/024,607_   CRF Processing Date: _1/22/2002_
                                         Edited by: _____
                                         Verified by: _____ (STIC staff)

ENTERED

#2

☐ Changed a file from non-ASCII to ASCII.

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: _Seqs. 9, 32 — inserted hard return_
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING   DATE: 01/22/2002
PATENT APPLICATION: US/10/024,607   TIME: 19:28:41

Input Set : A:\Pto.amc
Output Set: N:\CRF3\01222002\J024607.raw

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     5 <120> TITLE OF INVENTION: CARDIOVASCULAR DISEASE DIAGNOSTIC AND THERAPEUTIC TARGETS
     7 <130> FILE REFERENCE: B0801/7231/ERP/KA
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/024,607
C--> 9 <141> CURRENT FILING DATE: 2001-11-08
     9 <150> PRIOR APPLICATION NUMBER: US 60/247,457
    10 <151> PRIOR FILING DATE: 2000-11-09
    12 <160> NUMBER OF SEQ ID NOS: 33
    14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
    16 <210> SEQ ID NO: 1
    17 <211> LENGTH: 2586
    18 <212> TYPE: DNA
    19 <213> ORGANISM: Rattus norvegicus
    21 <220> FEATURE:
    22 <221> NAME/KEY: mRNA
    23 <222> LOCATION: (1)...(2586)
    24 <223> OTHER INFORMATION: Fit-1S
    26 <400> SEQUENCE: 1
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    28  cttcccagcc cttcatctgg gctacactga tttctctttt ggaccctaca tcagacagca     120
    29  cacatcaacc gcctagtgga ctcaccgtta ccttcctgtg ccattgccat cggagagatc     180
    30  tcggccatca atcactagca catgattggc aaatggagaa tggggctttg ggctttggca     240
    31  attctgacag ttcccatgta tttcatagtg acagagggca gaaaaacatc ctggggtcta     300
    32  gaaaacgagg ctttaattgt cagatgcccc caaagaggag gtgcgattaa ccctgtggaa     360
    33  tggtattatt caaatacaaa tgaaagaatt cctactcaaa agagaaatcg gatcttcgtc     420
    34  tcaagagatc gtctgaagtt tctaccagcc aaagtggaag actctgggat ttatacgtgt     480
    35  gttatcagaa gccctgaatc gattaagacc ggatctttga atgtcaccat atataaaaga     540
    36  ccaccaaact gcaaaatccc tgattacatg atgtactcga cagtagatgg atcagataaa     600
    37  aattccaaga taacatgtcc aacaattgcc ttgtataatt ggacagcgcc tgttcagtgg     660
    38  tttaagaact gcaaagctct ccaagggcca aggttcaggg cacacatgtc ctatttgttc     720
    39  attgacaaag tgagtcatgt tgatgaaggt gactacacat gtcgattcac tcacacggag     780
    40  aacggaacca attacattgt gactgccacc agatcattca cagttgaaga aaaaggcttc     840
    41  tctacatttc cagtaattac aaaccctcca cacaactaca cagtggaagt ggaaatagga     900
    42  aaaacagcaa acattgcctg ctcagcttgc tttggcacag cctctcagtt cgttgctgtc     960
    43  ctgtggcaga ttaacaaaac gagaattgga tcttttggca aagcaagaat tcaagaagag    1020
    44  aaaggcccaa ataaaagttc cagcaatggc atgatttgct taacctcact gttaaggata    1080
    45  actggtgtga ccgacaagga cttctccctg aaatatgact gtgtggccat gaaccatcac    1140
    46  ggagtgataa ggcaccccgt aagactgaga aggaaacaac caagtaagga gtgtctctca    1200
    47  caaattgctt gacaaaattg gctgaatttg ctgcaaacca caatcctttt tctcagagga    1260
    48  ctgtgtgtta tagcttggtc ccaggggatt catcatgatc gtgggattag ttggccagtt    1320
    49  tcctcaaatg tgttttttcat gttgagaaag ctccttaaat ctggtctgtc cagaatgttt    1380
    50  ctgtcttcta gaaggactct ctgtcattgt atctttcctc tctctgtttc cccttgtcct    1440
    51  tgttctcctc acggtcctcc ccatcccttc accttccttc acgttctctc tactcttctt    1500
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RAW SEQUENCE LISTING   DATE: 01/22/2002
PATENT APPLICATION: US/10/024,607   TIME: 19:28:41

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Output Set: **N:\CRF3\01222002\J024607.raw**

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54  cccctttgtga ctcttgtaac agaaaacaac ttacacatta ggtggatgac caacttgatc  1680
55  ccattttaaa agagtagaga aaacatgata ttttaccct taacactctc ttatgatact    1740
56  aaccactgcc tcaatggcaa tacaactaat gtaaaaacat tattttaact tctttcaaat   1800
57  atcaagaggg tgtggaaggg agagagacac tgactctaag ctcatagtga tatgtggggc   1860
58  atttattggg attaagatat tgattaaatg attagggtgg gggtacctat tggataccat   1920
59  caagctgtgt cactgcctga agtggtagtt gggattttt tttggttctg tttgtcttct    1980
60  ttggtttgtt ttaactatag agaccattct gctcttgaac tcctagagtt ccacctggct    2040
61  ttgcctctca ggtcctggga ttaaagccat atgtcacctt acccagccag gatgtttctt   2100
62  gttttggttt caattttaga gcctctggct tgtaagattt ttataaagta gagtttgatt   2160
63  cataggtggc cagagttgtg actcatagat gggttttagt gaggtcttag gcatccaccc   2220
64  cttataatgc tgttacccag ggtgactgtg gaccacagca ctgtgttatg agatggtgga   2280
65  ggtcatggca cattctatag gaaaagagaa gccaagcccc tagtctcacc aggcacaacc   2340
66  ttgagtcctc actgctctcc tctgccaaca ggaccttttg tccagatttc tgagtattct   2400
67  ctagttacat ttgtatttga actatatttg tgttatctgt aattctgtat ttgtttgtt    2460
68  tgtgtgtggt tttgtatttt ccagattatt tttaattcac ctgttgctat tcaaatcaat   2520
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70  atgata                                                               2586
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74  <212> TYPE: PRT
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79  <222> LOCATION: (1)...(336)
80  <223> OTHER INFORMATION: Fit-1S
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86              20                  25                  30
87  Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Gly Ala
88              35                  40                  45
89  Ile Asn Pro Val Glu Trp Tyr Tyr Ser Asn Thr Asn Glu Arg Ile Pro
90      50                  55                  60
91  Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
92  65                  70                  75                  80
93  Leu Pro Ala Lys Val Glu Asp Ser Gly Ile Tyr Thr Cys Val Ile Arg
94              85                  90                  95
95  Ser Pro Glu Ser Ile Lys Thr Gly Ser Leu Asn Val Thr Ile Tyr Lys
96              100                 105                 110
97  Arg Pro Pro Asn Cys Lys Ile Pro Asp Tyr Met Met Tyr Ser Thr Val
98              115                 120                 125
99  Asp Gly Ser Asp Lys Asn Ser Lys Ile Thr Cys Pro Thr Ile Ala Leu
100         130                 135                 140
101 Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
102 145                 150                 155                 160
103 Gln Gly Pro Arg Phe Arg Ala His Met Ser Tyr Leu Phe Ile Asp Lys
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104                   165                  170                     175
105  Val Ser His Val Asp Glu Gly Asp Tyr Thr Cys Arg Phe Thr His Thr
106                   180                  185                  190
107  Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
108              195                  200                  205
109  Glu Glu Lys Gly Phe Ser Thr Phe Pro Val Ile Thr Asn Pro Pro His
110         210                  215                  220
111  Asn Tyr Thr Val Glu Val Glu Ile Gly Lys Thr Ala Asn Ile Ala Cys
112  225                  230                  235                  240
113  Ser Ala Cys Phe Gly Thr Ala Ser Gln Phe Val Ala Val Leu Trp Gln
114              245                  250                  255
115  Ile Asn Lys Thr Arg Ile Gly Ser Phe Gly Lys Ala Arg Ile Gln Glu
116              260                  265                  270
117  Glu Lys Gly Pro Asn Lys Ser Ser Ser Asn Gly Met Ile Cys Leu Thr
118         275                  280                  285
119  Ser Leu Leu Arg Ile Thr Gly Val Thr Asp Lys Asp Phe Ser Leu Lys
120         290                  295                  300
121  Tyr Asp Cys Val Ala Met Asn His His Gly Val Ile Arg His Pro Val
122  305                  310                  315                  320
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128  <212> TYPE: DNA
129  <213> ORGANISM: Rattus norvegicus
131  <220> FEATURE:
132  <221> NAME/KEY: mRNA
133  <222> LOCATION: (1)...(2065)
134  <223> OTHER INFORMATION: Fit-1M
136  <400> SEQUENCE: 3
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139  agatgcacct acccggcagg ggtgaaatcc caagctacac tgatttctct tttggaccct     180
140  acatcagaca gcacacatca accgcctagt ggactcaccg ttacttcct gtgccattgc      240
141  catcggagag atctcggcca tcaatcacta gcacatgatt ggcaaatgga gaatggggct     300
142  ttgggctttg gcaattctga cagttcccat gtatttcata gtgacagagg gcagaaaaac     360
143  atcctggggt ctagaaaacg aggctttaat tgtcagatgc ccccaaagag gaggtgcgat     420
144  taaccctgtg gaatggtatt attcaaatac aaatgaaaga attcctactc aaaagagaaa     480
145  tcggatcttc gtctcaagag atcgtctgaa gtttctacca gccaaagtgg aagactctgg     540
146  gatttatacg tgtgttatca gaagccctga atcgattaag accggatctt tgaatgtcac     600
147  catatataaa agaccaccaa actgcaaaat ccctgattac atgatgtact cgacagtaga     660
148  tggatcagat aaaaattcca agataacatg tccaacaatt gccttgtata attggacagc     720
149  gcctgttcag tggtttaaga actgcaaagc tctccaaggg ccaaggttca gggcacacat     780
150  gtcctatttg ttcattgaca aagtgagtca tgttgatgaa ggtgactaca catgtcgatt     840
151  cactcacacg gagaacggaa ccaattacat tgtgactgcc accagatcat tcacagttga     900
152  agaaaaggc ttctctacat ttccagtaat tacaaaccct ccacacaact acacagtgga      960
153  agtggaaata ggaaaaacag caaacattgc ctgctcagct tgctttggca cagcctctca    1020
154  gttcgttgct gtcctgtggc agattaacaa aacgagaatt ggatcttttg caaagcaag     1080
155  aattcaagaa gagaaaggcc caaataaaag ttccagcaat ggcatgattt gcttaacctc    1140
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RAW SEQUENCE LISTING   DATE: 01/22/2002
PATENT APPLICATION: US/10/024,607   TIME: 19:28:41

Input Set : A:\Pto.amc
Output Set: N:\CRF3\01222002\J024607.raw

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158  ccaccaaagc acctactaca tagttgccgg atgtagttta ttgctaatgt ttatcaatgt  1320
159  cttggtgata gtcttaaaag tgttctggat tgaggttgct ctgttctgga gagatataat  1380
160  ggcaccttac aaaacccaga atgatggaaa gctctatgat gcttacatca tttaccctcg  1440
161  ggtcttccgg ggcagcgcag cagggaccgg ctctgtggag tactttgttc actacactct  1500
162  gcccgacgtt ctcgaaaata aatgtggcta caagttgtgc atttacggga gagacctgct  1560
163  gcctgggcaa gatgcggcca ctgtggtgga aagcagtatc cagaatagta gacggcaagt  1620
164  gtttgtcctg gcccctcaca tgatgcacag caaagagttt gcctatgagc aggagatcgc  1680
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167  aatgcagggg accatcaagt ggagggaaga ccacgtggcc gacaaacagt ctctaagctc  1860
168  caaattctgg aagcatgtga ataccaaat gccagtcccg aaaagacccc ccaagatggc   1920
169  atctgttgcc gctccgttga gtggcaaggt gtgcttggac ctgaaacact tttgagtcgt  1980
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174  <211> LENGTH: 566
175  <212> TYPE: PRT
176  <213> ORGANISM: Rattus norvegicus
178  <220> FEATURE:
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181  <223> OTHER INFORMATION: Fit-1M
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187              20                  25                  30
188  Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Gly Ala
189          35                  40                  45
190  Ile Asn Pro Val Glu Trp Tyr Tyr Ser Asn Thr Asn Glu Arg Ile Pro
191      50                  55                  60
192  Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
193  65                  70                  75                  80
194  Leu Pro Ala Lys Val Glu Asp Ser Gly Ile Tyr Thr Cys Val Ile Arg
195                  85                  90                  95
196  Ser Pro Glu Ser Ile Lys Thr Gly Ser Leu Asn Val Thr Ile Tyr Lys
197              100                 105                 110
198  Arg Pro Pro Asn Cys Lys Ile Pro Asp Tyr Met Met Tyr Ser Thr Val
199              115                 120                 125
200  Asp Gly Ser Asp Lys Asn Ser Lys Ile Thr Cys Pro Thr Ile Ala Leu
201          130                 135                 140
202  Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
203  145                 150                 155                 160
204  Gln Gly Pro Arg Phe Arg Ala His Met Ser Tyr Leu Phe Ile Asp Lys
205                  165                 170                 175
206  Val Ser His Val Asp Glu Gly Asp Tyr Thr Cys Arg Phe Thr His Thr
207              180                 185                 190
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208  Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
209          195                 200                 205
210  Glu Glu Lys Gly Phe Ser Thr Phe Pro Val Ile Thr Asn Pro Pro His
211      210                 215                 220
212  Asn Tyr Thr Val Glu Val Glu Ile Gly Lys Thr Ala Asn Ile Ala Cys
213  225                 230                 235                 240
214  Ser Ala Cys Phe Gly Thr Ala Ser Gln Phe Val Ala Val Leu Trp Gln
215              245                 250                 255
216  Ile Asn Lys Thr Arg Ile Gly Ser Phe Gly Lys Ala Arg Ile Gln Glu
217              260                 265                 270
218  Glu Lys Gly Pro Asn Lys Ser Ser Ser Asn Gly Met Ile Cys Leu Thr
219          275                 280                 285
220  Ser Leu Leu Arg Ile Thr Gly Val Thr Asp Lys Asp Phe Ser Leu Lys
221          290                 295                 300
222  Tyr Asp Cys Val Ala Met Asn His His Gly Val Ile Arg His Pro Val
223  305                 310                 315                 320
224  Arg Leu Arg Arg Lys Gln Pro Ile Asp His Gln Ser Thr Tyr Tyr Ile
225              325                 330                 335
226  Val Ala Gly Cys Ser Leu Leu Leu Met Phe Ile Asn Val Leu Val Ile
227              340                 345                 350
228  Val Leu Lys Val Phe Trp Ile Glu Val Ala Leu Phe Trp Arg Asp Ile
229          355                 360                 365
230  Met Ala Pro Tyr Lys Thr Gln Asn Asp Gly Lys Leu Tyr Asp Ala Tyr
231          370                 375                 380
232  Ile Ile Tyr Pro Arg Val Phe Arg Gly Ser Ala Ala Gly Thr Gly Ser
233  385                 390                 395                 400
234  Val Glu Tyr Phe Val His Tyr Thr Leu Pro Asp Val Leu Glu Asn Lys
235              405                 410                 415
236  Cys Gly Tyr Lys Leu Cys Ile Tyr Gly Arg Asp Leu Leu Pro Gly Gln
237              420                 425                 430
238  Asp Ala Ala Thr Val Val Glu Ser Ser Ile Gln Asn Ser Arg Arg Gln
239          435                 440                 445
240  Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu Phe Ala Tyr
241          450                 455                 460
242  Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn Asn Ser Lys
243  465                 470                 475                 480
244  Val Ile Leu Ile Glu Met Glu Pro Met Gly Glu Ala Ser Arg Leu Gln
245              485                 490                 495
246  Leu Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys Met Gln Gly
247              500                 505                 510
248  Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln Ser Leu Ser
249              515                 520                 525
250  Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val Pro Lys Arg
251          530                 535                 540
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253  545                 550                 555                 560
254  Leu Asp Leu Lys His Phe
255                  565
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VERIFICATION SUMMARY   DATE: 01/22/2002
PATENT APPLICATION: **US/10/024,607**   TIME: 19:28:42

Input Set : **A:\Pto.amc**
Output Set: **N:\CRF3\01222002\J024607.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26